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<120> Nucleic Acids That Control Plant Development

<130> 023070-099910US

<140> US 09/840,743

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<160> 119

<170> PatentIn Ver. 2.1

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Gly	Asn	Lys	Asp	Met	Ser	Gly	Leu	Asp	His	Leu	Ser	Phe	Gly	Asp	Leu	50	55	60
Leu	Ala	Leu	Ala	Asn	Thr	Ala	Ser	Leu	Ile	Phe	Ser	Gly	Gln	Thr	Pro	65	70	75
Ile	Pro	Thr	Arg	Asn	Thr	Glu	Val	Met	Gln	Lys	Gly	Thr	Glu	Glu	Val	85	90	95
Glu	Ser	Leu	Ser	Ser	Val	Ser	Asn	Asn	Val	Ala	Glu	Gln	Ile	Leu	Lys	100	105	110
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Glu	Ala	Lys	Pro	Lys	Arg	Glu	Pro	Lys	Pro	Arg	Ala	Pro	Arg	Lys	Ser	130	135	140
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Arg	Lys	Lys	Val	Glu	Val	Ser	Lys	Asp	Gln	Asp	Ala	Thr	Pro	Val	Glu	165	170	175
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 645 650 655
 Ser Ser Pro Pro Asp His Asn His Ser Ser Val Thr Leu Lys Asn Thr
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 Arg Leu Ser Leu Glu Asn Leu Pro Gly Leu Tyr Asn Met Ser Cys Thr
 50 55 60
 Gln Leu Leu Ala Leu Ala Asn Ala Thr Val Ala Thr Gly Ser Ser Ile
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 Ile Asn Ser Trp Lys Met Asp Ser Asn Pro Trp Thr Leu Ser Lys Met
 100 105 110
 Gln Lys Gln Gln Tyr Asp Val Ser Thr Pro Gln Lys Phe Leu Cys Asp
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 130 135 140
 Glu Pro Glu Ser Pro Gln Ile Thr Leu Lys Thr Pro Gly Lys Ser Leu
 145 150 155 160
 Ser Glu Thr Asp His Glu Pro His Asp Arg Ile Lys Lys Ser Val Leu
 165 170 175
 Gly Thr Gly Ser Pro Ala Ala Val Lys Lys Arg Lys Ile Ala Arg Asn
 180 185 190
 Asp Glu Lys Ser Gln Leu Glu Thr Pro Thr Leu Lys Arg Lys Lys Ile
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 Arg Pro Lys Val Val Arg Glu Gly Lys Thr Lys Lys Ala Ser Ser Lys
 210 215 220
 Ala Gly Ile Lys Lys Ser Ser Ile Ala Ala Thr Ala Thr Lys Thr Ser
 225 230 235 240
 Glu Glu Ser Asn Tyr Val Arg Pro Lys Arg Leu Thr Arg Arg Ser Ile
 245 250 255
 Arg Phe Asp Phe Asp Leu Gln Glu Glu Asp Glu Glu Phe Cys Gly Ile
 260 265 270
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 275 280 285
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 Gln Arg Ser Ile Met Ala Thr Arg Pro Arg Asn Phe Arg Ser Leu Lys
 355 360 365
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 Tyr Glu Glu Gln Lys Ala Ile Val Lys Tyr Ser Lys Lys Gln Lys Pro
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 Lys Trp Trp Glu Glu Glu Arg Asn Met Phe His Gly Arg Ala Asn Ser
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 Trp Lys Gly Ser Val Val Asp Ser Val Val Gly Val Phe Leu Thr Gln
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 930 935 940
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Ser Gly Lys Arg Lys Tyr Val Arg Lys Lys Thr Ser Pro Gly Gln Pro
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Arg	Lys	Glu	Leu	Lys	Pro	Gly	Glu	Lys	Pro	Lys	Pro	Arg	Gly	Arg	Pro	740	745		750
Arg	Lys	Gly	Lys	Val	Val	Gly	Gly	Glu	Leu	Ala	Ser	Lys	Asp	Ser	His	755	760	765	
Thr	Asn	Pro	Leu	Gln	Asn	Glu	Ser	Thr	Ser	Cys	Ser	Tyr	Gly	Pro	Tyr	770	775	780	

Ala Gly Glu Ala Ser Val Gly Arg Ala Val Lys Ala Asn Arg Val Gly	785	790	795	800
Glu Asn Ile Ser Gly Ala Met Val Ser Leu Leu Asp Ser Leu Asp Ile		805	810	815
Val Ile Gln Lys Ile Lys Val Leu Asp Ile Asn Lys Ser Glu Asp Pro		820	825	830
Val Thr Ala Glu Pro His Gly Ala Leu Val Pro Tyr Asn Gly Glu Phe		835	840	845
Gly Pro Ile Val Pro Phe Glu Gly Lys Val Lys Arg Lys Arg Ser Arg	850	855	860	
Ala Lys Val Asp Leu Asp Pro Val Thr Ala Leu Met Trp Lys Leu Leu	865	870	875	880
Met Gly Pro Asp Met Ser Asp Cys Ala Glu Gly Met Asp Lys Asp Lys		885	890	895
Glu Lys Trp Leu Asn Glu Glu Arg Lys Ile Phe Gln Gly Arg Val Asp		900	905	910
Ser Phe Ile Ala Arg Met His Leu Val Gln Gly Asp Arg Arg Phe Ser		915	920	925
Pro Trp Lys Gly Ser Val Val Asp Ser Val Val Gly Val Phe Leu Thr	930	935	940	
Gln Asn Val Ser Asp His Leu Ser Ser Ser Ala Phe Met Ala Leu Ala	945	950	955	960
Ala Lys Phe Pro Val Lys Pro Glu Ala Ser Glu Lys Pro Ala Asn Val		965	970	975
Met Phe His Thr Ile Ser Glu Asn Gly Asp Cys Ser Gly Leu Phe Gly		980	985	990
Asn Ser Val Lys Leu Gln Gly Glu Ile Leu Val Gln Glu Ala Ser Asn	995	1000	1005	
Thr Ala Ala Ser Phe Ile Thr Thr Glu Asp Lys Glu Gly Ser Asn Ser	1010	1015	1020	
Val Glu Leu Leu Gly Ser Ser Phe Gly Asp Gly Val Asp Gly Ala Ala	1025	1030	1035	1040
Gly Val Tyr Ser Asn Ile Tyr Glu Asn Leu Pro Ala Arg Leu His Ala		1045	1050	1055
Thr Arg Arg Pro Val Val Gln Thr Gly Asn Ala Val Glu Ala Glu Asp		1060	1065	1070
Gly Ser Leu Glu Gly Val Val Ser Ser Glu Asn Ser Thr Ile Ser Ser	1075	1080	1085	
Gln Asn Ser Ser Asp Tyr Leu Phe His Met Ser Asp His Met Phe Ser	1090	1095	1100	

Ser Met Leu Leu Asn Phe Thr Ala Glu Asp Ile Gly Ser Arg Asn Met
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 Pro Lys Ala Thr Arg Thr Thr Tyr Thr Glu Leu Leu Arg Met Gln Glu
 1125 1130 1135
 Leu Lys Asn Lys Ser Asn Glu Thr Ile Glu Ser Ser Glu Tyr His Gly
 1140 1145 1150
 Val Pro Val Ser Cys Ser Asn Asn Ile Gln Val Leu Asn Gly Ile Gln
 1155 1160 1165
 Asn Ile Gly Ser Lys His Gln Pro Leu His Ser Ser Ile Ser Tyr His
 1170 1175 1180
 Gln Thr Gly Gln Val His Leu Pro Asp Ile Val His Ala Ser Asp Leu
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 Glu Gln Ser Val Tyr Thr Gly Leu Asn Arg Val Leu Asp Ser Asn Val
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 Thr Gln Thr Ser Tyr Tyr Pro Ser Pro His Pro Gly Ile Ala Cys Asn
 1220 1225 1230
 Asn Glu Thr Gln Lys Ala Asp Ser Leu Ser Asn Met Leu Tyr Gly Ile
 1235 1240 1245
 Asp Arg Ser Asp Lys Thr Thr Ser Leu Ser Glu Pro Thr Pro Arg Ile
 1250 1255 1260
 Asp Asn Cys Phe Gln Pro Leu Ser Ser Glu Lys Met Ser Phe Ala Arg
 1265 1270 1275 1280
 Glu Gln Ser Ser Ser Glu Asn Tyr Leu Ser Arg Asn Glu Ala Glu Ala
 1285 1290 1295
 Ala Phe Val Lys Gln His Gly Thr Ser Asn Val Gln Gly Asp Asn Thr
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 Val Arg Thr Glu Gln Asn Gly Gly Glu Asn Ser Gln Ser Gly Tyr Ser
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 Gln Gln Asp Asp Asn Val Gly Phe Gln Thr Ala Thr Thr Ser Asn Leu
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 Tyr Ser Ser Asn Leu Cys Gln Asn Gln Lys Ala Asn Ser Glu Val Leu
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 His Gly Val Ser Ser Asn Leu Ile Glu Asn Ser Lys Asp Asp Lys Lys
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 Thr Ser Pro Lys Val Pro Val Asp Gly Ser Lys Ala Lys Arg Pro Arg
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 Val Gly Ala Gly Lys Lys Lys Thr Tyr Asp Trp Asp Met Leu Arg Lys
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 Glu Val Leu Tyr Ser His Gly Asn Lys Glu Arg Ser Gln Asn Ala Lys
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Asp Ser Ile Asp Trp Glu Thr, Ile Arg Gln Ala Glu Val Lys Glu Ile
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 Ser Asp Thr Ile Arg Glu Arg Gly Met Asn Asn Met Leu Ala Glu Arg
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 Ile Lys Asp Phe Leu Asn Arg Leu Val Arg Asp His Gly Ser Ile Asp
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 Leu Glu Trp Leu Arg Tyr Val Asp Ser Asp Lys Ala Lys Asp Tyr Leu
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 Ile Cys Val Arg Leu Gly Trp Val Pro Leu Gln Pro Leu Pro Glu Ser
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 Leu Gln Leu His Leu Leu Glu Met Tyr Pro Met Leu Glu Asn Ile Gln
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 Lys Tyr Leu Trp Pro Arg Leu Cys Lys Leu Asp Gln Arg Thr Leu Tyr
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 Glu Leu His Tyr Gln Met Ile Thr Phe Gly Lys Val Phe Cys Thr Lys
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 Ser Lys Pro Asn Cys Asn Ala Cys Pro Met Arg Ala Glu Cys Lys His
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 Glu Lys Ser Leu Val Thr Ser Gly Thr Pro Ile Ala Ala Glu Thr Phe
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 His Gln Thr Tyr Ile Ser Ser Arg Pro Val Val Ser Gln Leu Glu Trp
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 Glu Cys Ala Ile Glu Asp Ser Phe Val Asp Asp Pro Glu Glu Ile Pro
 1685 1690 1695
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 Met Gln Ala Asn Asn Ile Glu Ile Glu Asp Ala Asp Met Ser Lys Ala
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 Leu Val Ala Ile Thr Pro Glu Val Ala Ser Ile Pro Thr Pro Lys Leu
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Lys Asn Val Ser Arg Leu Arg Thr Glu His Gln Val Tyr Glu Leu Pro
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 Asp Ser His Pro Leu Leu Glu Gly Phe Asn Gln Arg Glu Pro Asp Asp
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 Pro Cys Pro Tyr Leu Leu Ser Ile Trp Thr Pro Gly Glu Thr Ala Gln
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 Ser Thr Asp Ala Pro Lys Ser Val Cys Asn Ser Gln Glu Asn Gly Glu
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 Met Arg Gly Ser Phe Pro Leu Asn Gly Thr Tyr Phe Gln Val Asn Glu
 1845 1850 1855
 Val Phe Ala Asp His Asp Ser Ser Arg Asn Pro Ile Asp Val Pro Arg
 1860 1865 1870
 Ser Trp Ile Trp Asn Leu Pro Arg Arg Thr Val Tyr Phe Gly Thr Ser
 1875 1880 1885
 Ile Pro Thr Ile Phe Lys Gly Leu Thr Thr Glu Glu Ile Gln His Cys
 1890 1895 1900
 Phe Trp Arg Gly Phe Val Cys Val Arg Gly Phe Asp Arg Thr Ser Arg
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 1925 1930 1935
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 1940 1945 1950

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 Glu Thr Gln Thr Arg Thr Ser Ala Val Val Ser Ser Glu Lys Glu Ser
 35 40 45

Ala	Asn	Ser	Phe	Val	Pro	His	Asn	Gly	Thr	Gly	Leu	Val	Glu	Arg	Ile	50	55	60
Ser	Asn	Asp	Ala	Gly	Leu	Thr	Glu	Val	Val	Gly	Ser	Ser	Ala	Gly	Pro	65	70	75
Thr	Glu	Cys	Ile	Asp	Leu	Asn	Lys	Thr	Pro	Ala	Arg	Lys	Pro	Lys	Lys	85	90	95
Lys	Lys	His	Arg	Pro	Lys	Val	Leu	Lys	Asp	Asp	Lys	Pro	Ser	Lys	Thr	100	105	110
Pro	Lys	Ser	Ala	Thr	Pro	Ile	Pro	Ser	Thr	Glu	Lys	Val	Glu	Lys	Pro	115	120	125
Ser	Gly	Lys	Arg	Lys	Tyr	Val	Arg	Lys	Lys	Thr	Ser	Pro	Gly	Gln	Pro	130	135	140
Pro	Ala	Glu	Gln	Ala	Ala	Ser	Ser	His	Cys	Arg	Ser	Glu	Leu	Lys	Ser	145	150	155
Val	Lys	Arg	Ser	Leu	Asp	Phe	Gly	Gly	Glu	Val	Leu	Gln	Glu	Ser	Thr	165	170	175
Gln	Ser	Gly	Ser	Gln	Val	Pro	Val	Ala	Glu	Ile	Cys	Thr	Gly	Pro	Lys	180	185	190
Arg	Gln	Ser	Ile	Pro	Ser	Thr	Ile	Gln	Arg	Asp	Ser	Gln	Ser	Gln	Leu	195	200	205
Ala	Cys	His	Val	Val	Ser	Ser	Thr	Ser	Ser	Ile	His	Thr	Ser	Ala	Ser	210	215	220
Gln	Met	Val	Asn	Ala	His	Leu	Phe	Pro	Pro	Asp	Asn	Met	Pro	Asn	Gly	225	230	235
Val	Leu	Leu	Asp	Leu	Asn	Asn	Ser	Thr	Ser	Gln	Leu	Gln	Asn	Glu	His	245	250	255
Ala	Lys	Phe	Val	Asp	Ser	Pro	Ala	Arg	Leu	Phe	Gly	Ser	Arg	Ile	Arg	260	265	270
Gln	Thr	Ser	Gly	Lys	Asn	Ser	Leu	Leu	Glu	Ile	Tyr	Ala	Gly	Met	Ser	275	280	285
Asp	Arg	Asn	Val	Pro	Asp	Leu	Asn	Ser	Ser	Ile	Ser	Gln	Thr	His	Ser	290	295	300
Met	Ser	Thr	Asp	Phe	Ala	Gln	Tyr	Leu	Leu	Ser	Ser	Ser	Gln	Ala	Ser	305	310	315
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Pro	Glu	Asn	Pro	Ile	Thr	Pro	Ser	His	Cys	Ile	Glu	Arg	Ala	Ala	Leu	340	345	350
Lys	Glu	His	Leu	Asn	His	Val	Pro	His	Ala	Lys	Ala	Ala	Val	Met	Asn	355	360	365

Gly	Gln	Met	Pro	His	Ser	Tyr	Arg	Leu	Ala	Gln	Asn	Pro	Ile	Leu	Pro	370	375	380
Pro	Asn	His	Ile	Glu	Gly	Tyr	Gln	Val	Met	Glu	Asn	Leu	Ser	Glu	Leu	385	390	395
Val	Thr	Thr	Asn	Asp	Tyr	Leu	Thr	Ala	Ser	Pro	Phe	Ser	Gln	Thr	Gly	405	410	415
Ala	Ala	Asn	Arg	Gln	His	Asn	Ile	Gly	Asp	Ser	Met	His	Ile	His	Ala	420	425	430
Leu	Asp	Pro	Arg	Arg	Glu	Ser	Asn	Ala	Ser	Ser	Gly	Ser	Trp	Ile	Ser	435	440	445
Leu	Gly	Val	Asn	Phe	Asn	Gln	Gln	Asn	Asn	Gly	Trp	Ala	Ser	Ala	Gly	450	455	460
Ala	Ala	Asp	Ala	Ala	Ser	Ser	His	Ala	Pro	Tyr	Phe	Ser	Glu	Pro	His	465	470	475
Lys	Arg	Met	Arg	Thr	Ala	Tyr	Leu	Asn	Asn	Tyr	Pro	Asn	Gly	Val	Val	485	490	495
Gly	His	Phe	Ser	Thr	Ser	Ser	Thr	Asp	Leu	Ser	Asn	Asn	Glu	Asn	Glu	500	505	510
Asn	Val	Ala	Ser	Ala	Ile	Asn	Ser	Asn	Val	Phe	Thr	Leu	Ala	Asp	Ala	515	520	525
Gln	Arg	Leu	Ile	Ala	Arg	Glu	Lys	Ser	Arg	Ala	Ser	Gln	Arg	Met	Ile	530	535	540
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His	Gln	His	Gly	Arg	Pro	Ala	Pro	His	Gly	Ser	Ala	Cys	Arg	Glu	Ser	565	570	575
Ile	Glu	Val	Pro	Asp	Lys	Gln	Phe	Gly	Leu	Met	Thr	Glu	Glu	Leu	Thr	580	585	590
Gln	Leu	Pro	Ser	Met	Pro	Asn	Asn	Pro	Gln	Arg	Glu	Lys	Tyr	Ile	Pro	595	600	605
Gln	Thr	Gly	Ser	Cys	Gln	Leu	Gln	Ser	Leu	Glu	His	Asp	Met	Val	Lys	610	615	620
Gly	His	Asn	Leu	Ala	Gly	Glu	Leu	His	Lys	Gln	Val	Thr	Ser	Pro	Gln	625	630	635
Val	Val	Ile	Gln	Ser	Asn	Phe	Cys	Val	Thr	Pro	Pro	Asp	Val	Leu	Gly	645	650	655
Arg	Arg	Thr	Ser	Gly	Glu	His	Leu	Arg	Thr	Leu	Ile	Ala	Pro	Thr	His	660	665	670
Ala	Ser	Thr	Cys	Lys	Asp	Thr	Leu	Lys	Ala	Leu	Ser	Cys	Gln	Leu	Glu	675	680	685

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Ser Ala Asp Val Pro Arg Thr Asp Asn His Gln Val Lys Val Ser Glu
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Glu Thr Val

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<212> DNA
<213> *Oryza sativa*

<220>
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<213> Zea mays

<220>

<223> corn DMT.1 660990 (688512 selclone ID)

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20 25 30

Glu Thr Gly Arg Leu Cys Gly Ser Ser Thr Cys Phe Ser Cys Asn Asn
35 40 45

Ile Arg Glu Met Gln Ala Gln Lys Val Arg Gly Thr Leu Leu Ile Pro
50 55 60

Cys Arg Thr Ala Met Arg Gly Ser Phe Pro Leu Asn Gly Thr Tyr Phe
 65 70 75 80
 Gln Val Asn Glu Val Phe Ala Asp His Cys Ser Ser Gln Asn Pro Ile
 85 90 95
 Asp Val Pro Arg Ser Trp Ile Trp Asp Leu Pro Arg Arg Thr Val Tyr
 100 105 110
 Phe Gly Thr Ser Val Pro Thr Ile Phe Arg Gly Leu Thr Thr Glu Glu
 115 120 125
 Ile Gln Arg Cys Phe Trp Arg Gly Phe Val Cys Val Arg Gly Phe Asp
 130 135 140
 Arg Thr Val Arg Ala Pro Arg Pro Leu Tyr Ala Arg Leu His Phe Pro
 145 150 155 160
 Val Ser Lys Val Val Arg Gly Lys Lys Pro Gly Ala Ala Arg Ala Glu
 165 170 175

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<220>
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<210> 22
 <211> 166
 <212> PRT
 <213> Zea mays

<220>
 <223> corn DMT.2 371537 (441428 selclone ID)

<220>
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 <222> (1)..(166)
 <223> Xaa = any amino acid

 <400> 22
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 20 25 30

 Ala Ser Ala Arg Leu Ala Leu Pro Ala Pro Gln Glu Glu Ser Leu Val
 35 40 45

 Lys Leu Ser Asn Pro Phe Ala Phe Gln Asn Ser Ser Met His Ala Met
 50 55 60

 Asn Ser Thr His Leu Pro Arg Leu Glu Gly Ser Ile His Ser Arg Glu
 65 70 75 80

 Phe Leu Pro Lys Asn Ser Glu Pro Ile Ile Glu Glu Pro Ala Ser Pro
 85 90 95

 Arg Glu Glu Arg Pro Pro Xaa Thr Met Glu Asn Asp Ile Glu Asp Phe
 100 105 110

 Tyr Glu Asp Gly Glu Ile Pro Thr Ile Lys Leu Asn Met Glu Ala Phe
 115 120 125

 Ala Gln Asn Leu Glu Asn Cys Ile Lys Glu Ser Asn Asn Glu Leu Gln
 130 135 140

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 145 150 155 160

 Ser Ile Pro Xaa Pro Lys
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<210> 23
 <211> 506
 <212> DNA
 <213> Zea mays

<220>
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 gaaagacctc cakaaacat ggaaaatgat attgaagatt tttatgaaga tggtgaaatc 360
 ccaacaataa agcttaacat ggaagctttt gcacaaaact tggagaattg cattaagaa 420
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 rcagcttcsa ttcctgkacc gaaact 506

<210> 24
 <211> 276
 <212> PRT
 <213> Zea mays

<220>
 <223> corn DMT.3 218853

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 Asp Pro Ser Pro Glu Pro Tyr Pro Ser His Ala Ser Pro Cys Ser Ala
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 Gln Cys Leu Val Val Arg Asp Ala Leu Leu Ala Phe His Gly Phe Pro
 35 40 45
 Glu Glu Phe Ala Ala Phe Arg Val Leu Arg Leu Gly Gly Leu Ser Pro
 50 55 60
 Asn Arg Asp Pro Arg Pro Ser Ser Pro Thr Val Leu Asp Gly Leu Val
 65 70 75 80
 Thr Thr Leu Leu Ser Gln Asn Thr Thr Asp Ala Ile Ser Arg Arg Ala
 85 90 95
 Phe Ala Ser Leu Lys Ala Ala Phe Pro Ser Trp Asp Gln Val Val Asp
 100 105 110
 Glu Glu Gly Lys Arg Leu Glu Asp Ala Ile Arg Cys Gly Gly Leu Ala
 115 120 125
 Ala Thr Lys Ala Ala Arg Ile Arg Ser Met Leu Arg Asp Val Arg Glu
 130 135 140
 Arg Arg Gly Lys Ile Cys Leu Glu Tyr Leu Arg Glu Leu Ser Val Asp
 145 150 155 160
 Glu Val Lys Lys Glu Leu Ser Arg Phe Lys Gly Ile Gly Pro Lys Thr
 165 170 175
 Val Ala Cys Val Leu Met Phe Tyr Leu Gln Lys Asp Asp Phe Pro Val
 180 185 190
 Asp Thr His Val Leu Arg Ile Thr Lys Ala Met Gly Trp Val Pro Ala
 195 200 205
 Thr Ala Ser Arg Glu Lys Ala Tyr Ile His Leu Asn Asn Lys Ile Pro
 210 215 220
 Asp Asp Leu Lys Phe Asp Leu Asn Cys Leu Phe Val Thr His Gly Lys
 225 230 235 240
 Leu Cys Gln Ser Cys Thr Lys Lys Val Gly Ser Asp Lys Arg Lys Ser
 245 250 255
 Ser Asn Ser Ala Cys Pro Leu Ala Gly Tyr Cys Cys Ile Gly Glu Lys
 260 265 270

Leu Gln Gln Leu
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<210> 25
<211> 183
<212> PRT
<213> Triticum sp.

<220>
<223> wheat DMT.1 614028 (887053 selclone ID)

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20 25 30
Pro Ile Ala Ser Gly Ser Cys Gln Gln Pro Tyr Ile Ser Ser Met Arg
35 40 45
Leu Asn Gln Leu Asp Trp Asn Ala Asn Ala His Asp His Ile Leu Asp
50 55 60
Asn Arg Gln Pro Ile Ile Glu Glu Pro Ala Ser Pro Glu Pro Glu Pro
65 70 75 80
Glu Thr Ala Glu Met Arg Glu Ser Ala Ile Glu Asp Ile Phe Leu Asp
85 90 95
Asp Pro Glu Glu Ile Pro Thr Ile Lys Leu Asn Phe Glu Glu Phe Ala
100 105 110
Gln Asn Leu Lys Asn Tyr Met Gln Val Asn Asn Ile Glu Met Glu Asp
115 120 125
Ala Asp Met Ser Ser Ala Leu Val Ala Ile Thr Pro Glu Ala Ala Ser
130 135 140
Ile Pro Thr Pro Arg Leu Lys Asn Val Ser Arg Leu Arg Thr Glu His
145 150 155 160
Gln Val Tyr Glu Leu Pro Asp Ser His Pro Leu Leu Glu Gly Tyr Asp
165 170 175
Gln Arg Glu Pro Asp Asp Pro
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<210> 26
<211> 557
<212> DNA
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<220>
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<210> 27
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 <213> Triticum sp.

<220>
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 Pro Lys Lys Thr Arg Thr Thr Arg Lys Lys Asn Thr Glu Asn Phe Asp
 20 25 30
 Trp Asp Lys Phe Arg Arg Gln Ala Cys Ala Asp Gly His Met Lys Glu
 35 40 45
 Arg Lys Ser Glu Arg Arg Asp Ser Val Asp Trp Glu Ala Val Arg Cys
 50 55 60
 Ala Asp Val Gln Arg Ile Ser Gln Ala Ile Arg Glu Arg Gly Met Asn
 65 70 75 80
 Asn Val Leu Ser Glu Arg Ile Gln Glu Phe Leu Asn Arg Leu Val Arg
 85 90 95
 Asp His Gly Ser Ile Asp Leu Glu Trp Leu Arg Asp Ile Pro Pro Asp
 100 105 110
 Ser Ala Lys Asp Tyr Leu Leu Ser Ile Arg Gly Leu Gly Leu Lys Ser
 115 120 125
 Val Glu Cys Val Arg Leu Leu Thr Leu His His Leu Ala Phe Pro Val
 130 135 140

Asp
 145

<210> 28
 <211> 439
 <212> DNA
 <213> Triticum sp.

<220>
 <223> wheat DMT.2 568842 (908118 selclone ID)

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 caagaaccac aagaaaaaaa aatactgaaa acttcgactg ggacaaattt cgaagacagg 120

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ataatgtttt atcagaacga atccaggaat tccctgaatcg cttgggttaga gatcatggaa 300
gcattgatct tgaatgggta agagatatcc cccctgactc agcaaaggac tacttgctta 360
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tcgctttccc tgtwgacac                                     439
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 <211> 108
 <212> PRT
 <213> Triticum sp.

<220>
 <223> wheat DMT.3 611792 (838515 selclone ID)

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 Asp Pro Ile Tyr Val Ala Arg Glu Gln Leu Trp Lys Leu Glu Arg Arg
 20 25 30
 Met Val Tyr Phe Gly Thr Ser Val Pro Ser Ile Phe Lys Gly Leu Thr
 35 40 45
 Thr Glu Glu Ile Gln Gln Cys Phe Trp Lys Gly Phe Val Cys Val Arg
 50 55 60
 Gly Phe Glu Arg Glu Thr Gly Ala Pro Arg Pro Leu Cys Gln His Leu
 65 70 75 80
 His Val Ala Ala Ser Lys Val Pro Arg Ser Arg Asn Ala Ala Ala Ala
 85 90 95
 Gly Leu Asn Ser Asp Ser Ala Lys Ala Ser Ala Pro
 100 105

<210> 30
 <211> 624
 <212> DNA
 <213> Triticum sp.

<220>
 <223> wheat DMT.3 611792 (838515 selclone ID)

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 gtctgtgtgc ggggattcga gagggaaacc ggggcaccaa ggcctctatg ccaacatctg 240
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 gattcagcaa aggcacgcgc tccatgagta tcatcacacc ggctatcgac ctgtgcatgg 360
 gtacgctagt gttggttcct gccgggcwac agccgttytt gtaggaaata aaccsctgcg 420
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 aatccctgtg agctytattg taccttgaat ttactttccg accagtttat ccgcttgcaa 540
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 ttgtcttgcc akacgacctt acgt 624

<210> 31
 <211> 145
 <212> PRT
 <213> Triticum sp.

<220>
 <223> wheat DMT.4 615131 (861906 selclone ID)

<400> 31
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 Leu Ala Leu Pro Ala Pro Gln Glu Lys Ser Leu Val Met Ser Ser Asn
 20 25 30
 Gln Phe Ser Phe Gln Ser Gly Gly Met Pro Thr Pro Tyr Ser Thr Val
 35 40 45
 Leu Pro Gln Leu Glu Gly Ser Ala Gln Gly Gln Asp Phe Cys Thr Asn
 50 55 60
 Asn Ser Glu Pro Ile Ile Glu Glu Pro Ala Ser Pro Ala Arg Glu Glu
 65 70 75 80
 Cys Pro Glu Thr Leu Glu Asn Asp Ile Glu Asp Tyr Asp Pro Asp Thr
 85 90 95
 Gly Glu Ile Pro Leu Ile Lys Leu Asn Leu Gln Ala Phe Ala Gln Asn
 100 105 110
 Leu Glu Asn Cys Ile Lys Glu Ser Asn Met Asp Leu Gly Ser Asp Asp
 115 120 125
 Ile Ala Lys Ala Leu Val Ala Val Ser Thr Gly Ser Ala Ser Ile Pro
 130 135 140
 Val
 145

<210> 32
 <211> 492
 <212> DNA
 <213> Triticum sp.

<220>
 <223> wheat DMT.4 615131 (861906 selclone ID)

<400> 32
 tacttttggga aaggtgttct gtacaaaaaa caagccaaat tgcaatgctt gtccaatgag 60
 aagcgaatgc aggcatttcg caagtgcctt cgcaagtgc cggcttgac ttctgcacc 120
 tcaggagaaa agtttggtga tgtcgagcaa tcaattcagt ttccagagt gtggcatgcc 180
 aactccatac tcaactgtgc ttctcagct tgaggggaagt gcccagggac aggatttttg 240
 cactaacaat tcagagccaa ttattgagga gccagcaagt ccagcacggg aagaatgtcc 300
 agaaactctt gaaaatgata ttgaagatta cgatccagat actggtgaaa tcccactaat 360
 taagcttaac ttgcaagctt ttgctcagaa cttggaaaac tgcattaaag aaagcaatat 420
 ggatcttggg tctgatgata tcgcaaaagc acttggtgct gtagcactg gatcagcttc 480
 aattcctgct cc 492

<210> 33
 <211> 298
 <212> PRT
 <213> Glycine max

<220>
 <223> soybean DMT.1 449122 (557119 selclone ID)

<220>
 <221> MOD_RES
 <222> (1)..(298)
 <223> Xaa = any amino acid

<400> 33
 Met Asp Ser Leu Asp Trp Asp Ala Val Arg Cys Ala Asp Val Ser Glu
 1 5 10 15
 Ile Ala Glu Thr Ile Lys Glu Arg Gly Met Asn Asn Arg Leu Ala Asp
 20 25 30
 Arg Ile Lys Asn Phe Leu Asn Arg Leu Val Glu Glu His Gly Ser Ile
 35 40 45
 Asp Leu Glu Trp Leu Arg Asp Val Pro Pro Asp Lys Ala Lys Glu Tyr
 50 55 60
 Leu Leu Ser Ile Arg Gly Leu Gly Leu Lys Ser Val Glu Cys Val Arg
 65 70 75 80
 Leu Leu Thr Leu His His Leu Ala Phe Pro Val Asp Thr Asn Val Gly
 85 90 95
 Arg Ile Ala Val Arg Leu Gly Trp Val Pro Leu Gln Pro Leu Pro Glu
 100 105 110
 Ser Leu Gln Leu His Leu Leu Glu Leu Tyr Pro Val Leu Glu Ser Ile
 115 120 125
 Gln Lys Tyr Leu Trp Pro Arg Leu Cys Lys Leu Asp Gln Glu Thr Leu
 130 135 140
 Tyr Glu Leu His Tyr Gln Met Ile Thr Phe Gly Lys Xaa Phe Cys Thr
 145 150 155 160
 Lys Ser Lys Pro Asn Cys Asn Ala Cys Pro Met Arg Xaa Glu Cys Arg
 165 170 175
 His Phe Ala Ser Ala Phe Ala Ser Ala Arg Phe Ala Leu Pro Gly Pro
 180 185 190
 Glu Gln Lys Ser Ile Val Ser Thr Thr Gly Asn Ser Val Ile Asn Gln
 195 200 205
 Asn Pro Ser Glu Ile Ile Ser Gln Leu His Leu Pro Pro Pro Glu Asn
 210 215 220
 Thr Ala Gln Glu Asp Glu Ile Gln Leu Thr Glu Val Ser Arg Gln Leu
 225 230 235 240
 Glu Ser Lys Phe Glu Ile Asn Ile Cys Gln Pro Ile Ile Glu Glu Pro
 245 250 255

Arg Thr Pro Glu Pro Glu Cys Leu Gln Glu Ser Gln Thr Asp Ile Glu
 260 265 270

Asp Ala Phe Tyr Glu Asp Ser Ser Glu Ile Pro Thr Ile Asn Leu Asn
 275 280 285

Ile Glu Glu Phe Thr Leu Asn Leu Gln Asn
 290 295

<210> 34
 <211> 638
 <212> DNA
 <213> Glycine max

<220>
 <223> soybean DMT.1 449122 (557119 selclone ID)

<400> 34
 aataaaattt aakagcaagg aacaagaaaa agagaaaaag gatgaytttg actgggatag 60
 tttaagaatt gaagcacagg ctaaggctgg gaaaagagaa aagacagata acaccatgga 120
 ttctttggac tgggatgctg tgagatgtgc agatgtcagt gaaatcgctg agaccatcaa 180
 agaaaggggc atgaacaaca ggcttgacaga tcgtattaag aatttcttaa atcgattggg 240
 tgaagaacat ggaagcattg accttgaatg gcttagagac gttccacctg acaaagcaaa 300
 agaatacttg ctcagcataa gaggattggg actaaaaagt gtggaatgtg tgcggctttt 360
 aacactgcac catcttgctt tcccggtaga cacaaatgtc ggacgtatag cagtacgact 420
 gggatgggtc cctctacagc cactgcctga gtcactgcag ttgcatctcc tagaattgta 480
 cccagtgttg gagtcaatac aaaaatatct ctggcctcga ctatgcaagc tagatcagga 540
 aacactatat gagctacatt accagatgat tacatttggg aaggkcttct gtacaaaaag 600
 caaaccaaat tgtaatgcat gcccaatgag aggagaat 638

<210> 35
 <211> 251
 <212> PRT
 <213> Glycine max

<220>
 <223> soybean DMT.2 387990 (473695 selclone ID)

<400> 35
 Met Arg Met Thr Ile Asp Leu Val Ser Gln Gln Ser Leu Thr Ala Arg
 1 5 10 15
 Leu Gln Leu Ser Ile Leu Lys Asp Lys Leu Lys Ile Gln Cys Arg Lys
 20 25 30
 Ala Arg Gly Leu Asp Phe Gly Arg Asn Glu Ser Ser Lys Ile Asp Ser
 35 40 45
 Ser Pro Val Lys Leu Arg Ser Arg Glu His Gly Lys Glu Lys Lys Asn
 50 55 60
 Asn Phe Asp Trp Asp Ser Leu Arg Ile Gln Ala Glu Ala Lys Ala Gly
 65 70 75 80
 Lys Arg Glu Lys Thr Glu Asn Thr Met Asp Ser Leu Asp Trp Asp Ala
 85 90 95
 Val Arg Arg Ala Asp Val Ser Glu Ile Ala Asn Ala Ile Lys Glu Arg
 100 105 110

Gly Met Asn Asn Met Leu Ala Glu Arg Ile Gln Ser Phe Leu Asn Leu
 115 120 125
 Leu Val Asp Lys His Gly Gly Ile Asp Leu Glu Trp Leu Arg Asp Val
 130 135 140
 Pro Pro Asp Gln Ala Lys Glu Phe Leu Leu Ser Ile Arg Gly Leu Gly
 145 150 155 160
 Leu Lys Ser Val Glu Cys Val Arg Leu Leu Thr Leu His His Leu Ala
 165 170 175
 Phe Pro Val Asp Thr Asn Val Gly Arg Ile Ala Val Arg Leu Gly Trp
 180 185 190
 Val Pro Leu Gln Pro Leu Pro Glu Ser Leu Gln Leu His Leu Leu Glu
 195 200 205
 Leu Tyr Pro Val Leu Glu Ser Ile Gln Lys Tyr Leu Trp Pro Arg Leu
 210 215 220
 Cys Lys Leu Asp Gln Arg Thr Leu Tyr Glu Leu His Tyr Gln Leu Ile
 225 230 235 240
 Thr Phe Gly Lys Val Phe Cys Thr Lys Ser Lys
 245 250

<210> 36
 <211> 1134
 <212> DNA
 <213> Glycine max

<220>
 <223> soybean DMT.2 387990 (473695 selclone ID)

<400> 36
 gaaaagatag gatcattctc agatagcaac tcagaaatag aagacctgtc tagcgctgcc 60
 aagtacaata gttattataa tagaatttct ttcagtgagc ttttagaaat ggcaagttca 120
 accatgttgc atgaagttaa cagtcaaaga agcaaataca ctgagaactt aggagataca 180
 tgtgatcagt ctatagacat gaagcatgac aacctggcag aaaacttggg aaaatcggat 240
 gttactcaag gctccgcaga agcacccatc accaatggat atacttttaa aataacccca 300
 aactcaggag tacttgaggt taactgttat gatcctctca aaatagaagt cccatcaagt 360
 ggctcctcaa agggtaaaga tgagaatgac aatagatcta gtttcccaac agagtctgac 420
 tgccaggctg caattgtcca ttctcaagga caaactgaag atccaatgca ggaaagcaag 480
 gggactagat tttggttaga atgaaagcag taagatagat tcttcccctg taaaattaag 540
 gagcagggag catggaaaag agaaaaagaa taactttgat tgggatagtt taagaatata 600
 agcagaagct aaggcagga aaagagaaaa gacagagaac accatggact ccttggaactg 660
 ggatgctgtt agacgcgcag atgtcagtga aattgccaat gcaatcaaag aaaggggcat 720
 gaacaacatg cttgctgaac gtattcagag tttcctgaat ctattgggtg acaagcatgg 780
 gggcatcgat cttgagtggc tgagagatgt tccacctgat caagcaaaaag aattcttgct 840
 cagcataagg ggattgggat tgaaaagtgt ggagtgtgta cgactcttaa cactacacca 900
 tcttgctctt ccggtggaca caaatgttgg acgtatagca gtaagattgg gatgggtgcc 960
 tctccagcca ctgccagagt cactacagtt gcattctcta gaattgtacc cagtgttgga 1020
 gtccatacaa aaatatctct ggccccggct ctgcaagcta gaccaaagaa cattgtatga 1080
 gctgcattac cagctgatta catttggaaa ggtcttctgt actaaaagca agcc 1134

<210> 37
 <211> 209
 <212> PRT
 <213> Glycine max

<220>
 <223> soybean DMT.3 657152 (546665 selclone ID)

<220>
 <221> MOD_RES
 <222> (1)..(209)
 <223> Xaa = any amino acid

<400> 37
 Ile Asn Gln Ala Glu Leu Gln Gln Thr Glu Val Ile Arg Gln Leu Glu
 1 5 10 15
 Ala Lys Ser Glu Ile Asn Ile Ser Gln Pro Ile Ile Glu Glu Pro Ala
 20 25 30
 Thr Pro Glu Pro Glu Cys Ser Gln Val Ser Glu Asn Asp Ile Glu Asp
 35 40 45
 Thr Phe Asn Glu Glu Ser Cys Glu Ile Pro Thr Ile Lys Leu Asp Ile
 50 55 60
 Glu Glu Phe Thr Leu Asn Leu Gln Asn Tyr Met Gln Glu Asn Met Glu
 65 70 75 80
 Leu Gln Glu Gly Glu Met Ser Lys Ala Leu Val Ala Leu His Pro Gly
 85 90 95
 Ala Ala Cys Ile Pro Thr Pro Lys Leu Lys Asn Val Ser Arg Leu Arg
 100 105 110
 Thr Glu His Tyr Val Tyr Glu Leu Pro Asp Ser His Pro Leu Leu Asn
 115 120 125
 Gly Trp Asn Lys Arg Glu Pro Asp Asp Pro Gly Lys Tyr Leu Leu Ala
 130 135 140
 Ile Trp Thr Pro Gly Glu Thr Ala Asx Ser Ile Gln Pro Pro Glu Ser
 145 150 155 160
 Lys Cys Ser Ser Gln Glu Glu Cys Gly Xaa Leu Cys Asn Glu Asn Glu
 165 170 175
 Cys Phe Ser Cys Asn Ser Phe Arg Glu Ala Xaa Phe Xaa Asp Ser Xaa
 180 185 190
 Arg Asp Thr Pro Asp Thr Met Ser Asn Ser Xaa Xaa Xaa Gly Ala Phe
 195 200 205

His

<210> 38
 <211> 616
 <212> DNA
 <213> Glycine max

<220>

<223> soybean DMT.3 657152 (546665 selclone ID)

<400> 38

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tataaaccaa gcagaacttc aacaaacaga agtgatcagg caactagaag caaaatctga 60
aatcaacatc agccaaccta ttattgaaga gccagcaact ccagagccag aatgctccca 120
agtatccgaa aatgatatag aggatacctt caatgaggaa tcatgtgaaa ttcccacat 180
caaaactagac atagaagagt tcactttgaa cttacaaaac tatatgcaag aaaacatgga 240
acttcaagaa ggtgaaatgt caaaggcctt ggttgctcta catccagggtg ctgcatgcat 300
tcctacaccc aagctgaaga atgtgagccg gttgcgaaca gagcattatg tttatgaact 360
ccctgattca catccccttc tgaatgggtg gaacaagcga gaacctgatg atccaggcaa 420
ataccttcta gctatatgga ctccagggga gacagcagat tctatacagc caccagaaaag 480
caaatgcagc tctcaggaat gtggccggct ctgtaatgag aatgaatggt tttcatgcaa 540
cagtttccgt gaagcaaggt tcacagatag ttcgaggga actcctgata ccatgtcgaa 600
cagctwtgar agggag 616
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<210> 39

<211> 102

<212> PRT

<213> Glycine max

<220>

<223> soybean DMT.4 432980 (663678 selclone ID)

<400> 39

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Glu Ala Ala Ser Ile Pro Met Pro Lys Leu Lys Asn Val Ser Arg Leu
  1             5             10             15

Arg Thr Glu His Cys Val Tyr Glu Leu Pro Asp Thr His Pro Leu Leu
          20             25             30

Gln Gly Trp Asp Thr Arg Glu Pro Asp Asp Pro Gly Lys Tyr Leu Leu
          35             40             45

Ala Ile Trp Thr Pro Gly Glu Thr Ala Asn Ser Ile Gln Pro Pro Glu
          50             55             60

Ser Lys Cys Ser Ser Gln Glu Glu Cys Gly Gln Leu Cys Asn Glu Asn
          65             70             75             80

Glu Cys Phe Ser Cys Asn Ser Phe Arg Glu Ala Asn Ser Gln Ile Val
          85             90             95

Arg Gly Thr Leu Leu Val
          100
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<210> 40

<211> 457

<212> DNA

<213> Glycine max

<220>

<223> soybean DMT.4 432980 (663678 selclone ID)

<400> 40

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agaagctgct tccattccta tgcccaagct aaagaatgtg agccgattac gaacagagca 60
ttgtgtttat gaactcccag atacgcatcc tttctccaa ggtgaggaca cagcagagcc 120
tgatgatcca ggcaaatatc ttcttgctat atggactcca ggtgagacag caaattctat 180
acagccacca gaaagcaaat gcagctctca agaagaatgt ggccaactct gtaatgagaa 240
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tgaatgtttc tcgtgcaaca gtttccgtga agcaaattct cagatagtta gagggacact 300
 cctgggtctga atgcttatca aaatcattgt tttaaccata tgtagcttac taattcttat 360
 acattatggg aacaggggag ggaatacatc tccatagaaa ttcaagcatt ataatagact 420
 gacttgaatt tatgataaat atgagcagat accatgt 457

<210> 41
 <211> 217
 <212> PRT
 <213> Medicago truncatula

<220>
 <223> Medicago 6654943

<400> 41
 Met Glu Leu Gln Glu Gly Glu Met Ser Lys Ala Leu Val Ala Leu Asn
 1 5 10 15
 Gln Glu Ala Ser Tyr Ile Pro Thr Thr Lys Leu Lys Asn Val Ser Arg
 20 25 30
 Leu Arg Thr Glu His Ser Val Tyr Glu Leu Pro Asp Ser His Pro Leu
 35 40 45
 Leu Glu Gly Trp Glu Lys Arg Glu Pro Asp Asp Pro Gly Lys Tyr Leu
 50 55 60
 Leu Ala Ile Trp Thr Pro Gly Glu Thr Ala Asn Ser Ile Gln Pro Pro
 65 70 75 80
 Asp Arg Arg Cys Ser Ala Gln Asp Cys Gly Gln Leu Cys Asn Glu Glu
 85 90 95
 Glu Cys Phe Ser Cys Asn Ser Phe Arg Glu Ala Asn Ser Gln Ile Val
 100 105 110
 Arg Gly Thr Ile Leu Ile Pro Cys Arg Thr Ala Met Arg Gly Ser Phe
 115 120 125
 Pro Leu Asn Gly Thr Tyr Phe Gln Val Asn Glu Val Phe Ala Asp His
 130 135 140
 Glu Ser Ser Leu Asn Pro Ile Ser Val Pro Arg Ser Leu Ile Trp Asn
 145 150 155 160
 Leu Asp Arg Arg Thr Val His Phe Gly Thr Ser Val Thr Ser Ile Phe
 165 170 175
 Lys Gly Leu Ala Thr Pro Glu Ile Gln Gln Cys Phe Trp Arg Gly Phe
 180 185 190
 Val Cys Val Arg Ser Phe Glu Arg Ser Thr Arg Ala Pro Arg Pro Leu
 195 200 205
 Met Ala Arg Leu His Phe Pro Ala Ser
 210 215

<210> 42
 <211> 657
 <212> DNA
 <213> Medicago truncatula

<220>
 <223> Medicago 6654943 EST306265

<400> 42
 gagaacatgg aacttcaaga aggtgaaatg tcaaaggcct tggttgctct aaatcaagaa 60
 gcttcttaca ttcctacaac gaagctgaag aacgtgagtc ggttgcgac agagcattct 120
 gtttatgaac tcccagattc tcatcctctt ctggaagggt gggaaaagcg agaacctgat 180
 gatccaggaa aataccttct agctatatgg acgccagggt agactgcaaa ttctatacag 240
 ccaccagaca gaagatgcag cgctcaagat tgtggccaac tctgtaatga ggaggaatgt 300
 ttttcgtgca acagcttccg tgaagcaaat tcacagatag ttcgagggac aatcctgata 360
 ccatgtcgaa cagctatgag agggagcttt cgcgtaaacg gaacctattt tcaagtcaat 420
 gaggtttttg cagaccatga atcaagtctt aatccgatta gcgttccag aagtttgata 480
 tggaaccttg ataggaggac agtgcatttt ggaacctccg taacaagcat attcaaagg 540
 ttagcaacac cagaaattca acagtgttc tggagagggt ttgtctgtgt gcggagcttt 600
 gaaagggtcaa cgagagcacc ccgtccttta atggccagac tgcatttccc agcaagc 657

<210> 43
 <211> 210
 <212> PRT
 <213> Lycopersicon esculentum

<220>
 <223> tomato 12624037

<400> 43
 Met Glu Leu Gln Glu Gly Glu Met Ser Lys Ala Leu Val Ala Leu Asn
 1 5 10 15
 Gln Glu Ala Ser Tyr Ile Pro Thr Thr Lys Leu Lys Asn Val Ser Arg
 20 25 30
 Leu Arg Thr Glu His Ser Val Tyr Glu Leu Pro Asp Ser His Pro Leu
 35 40 45
 Leu Glu Gly Trp Glu Lys Arg Glu Pro Asp Asp Pro Gly Lys Tyr Leu
 50 55 60
 Leu Ala Ile Trp Thr Pro Gly Glu Thr Ala Asn Ser Ile Gln Pro Pro
 65 70 75 80
 Asp Arg Arg Cys Ser Ala Gln Asp Cys Gly Gln Leu Cys Asn Glu Glu
 85 90 95
 Glu Cys Phe Ser Cys Asn Ser Phe Arg Glu Ala Asn Ser Gln Ile Val
 100 105 110
 Arg Gly Thr Ile Leu Ile Pro Cys Arg Thr Ala Met Arg Gly Ser Phe
 115 120 125
 Pro Leu Asn Gly Thr Tyr Phe Gln Val Asn Glu Val Phe Ala Asp His
 130 135 140
 Glu Ser Ser Leu Asn Pro Ile Ser Val Pro Arg Ser Leu Ile Trp Asn
 145 150 155 160

Leu Asp Arg Arg Thr Val His Phe Gly Thr Ser Val Thr Ser Ile Phe
165 170 175

Lys Gly Leu Ala Thr Pro Glu Ile Gln Gln Cys Phe Trp Arg Gly Phe
180 185 190

Val Cys Val Arg Ser Phe Glu Arg Ser Thr Arg Ala Pro Arg Pro Leu
195 200 205

Met Ala
210

<210> 44
<211> 758
<212> DNA
<213> Lycopersicon esculentum

<220>
<223> tomato 12624037 EST469495

<400> 44
gcttgagaaa ggaagtccaa tcaaagagtg ggaaaaaaga aagaagcaag gatgcaatgg 60
actcattgaa ctacgaagca gtcagaagtg cagcagttaa agaaatttct gatgctatta 120
aggaacgagg gatgaacaac atgctggcag agcgaattaa ggacttcctc gatagactgg 180
tgagggatca tgggaagtatt gacctagaat ggttgagaga tgtggcccca gacaaagcga 240
aagagtatct tttgagtatt cgtggactgg gtctgaaaag tgtagaatgt gtgcggctat 300
taacacttca taaccttgct tttccagttg acacaaatgt tggacgaata gctgtgagat 360
taggatgggt tcctctccaa ccacttcctg agtccctgca gttgcatctt cttgaactgt 420
atccaattct ggagtcaatt cagaagtatc tctggccacg actctgcaag ctcgatcaga 480
gaacactgta tgagttgcac taccacatga ttacctttgg aaagggtttc tgcacaaaaa 540
gtaagcctaa ctgtaatgca tgcccactga gagctgaatg cagacacttt gctagtgtct 600
acgcaagtgc aagacttgcc cttcctggcc cagaggagaa gagtatagtg agttcagcag 660
ttccgatccc tagtgaggga aatgcagctg ccgcattcaa gcccatgcta ttacccccag 720
agctgaagta gggatggcgt acccatatgc tccaattg 758

<210> 45
<211> 203
<212> PRT
<213> Hordeum vulgare

<220>
<223> barley 13256964

<220>
<221> MOD_RES
<222> (1)..(203)
<223> Xaa = any amino acid

<400> 45
Met Ala Ser Glu Thr Glu Thr Phe Ala Phe Gln Ala Glu Ile Asn Gln
1 5 10 15

Leu Leu Ser Leu Ile Ile Asn Thr Phe Tyr Ser Asn Lys Glu Ile Phe
20 25 30

Leu Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu Asp Lys Ile Arg
35 40 45

Phe Glu Ser Leu Thr Asp Lys Ser Lys Leu Asp Ala Gln Pro Glu Leu
 50 55 60
 Phe Ile His Ile Ile Pro Asp Lys Ala Thr Asn Thr Leu Thr Leu Ile
 65 70 75 80
 Asp Ser Gly Ile Gly Met Thr Lys Ser Asp Leu Val Asn Asn Leu Gly
 85 90 95
 Thr Ile Ala Arg Ser Gly Thr Lys Asp Phe Met Glu Ala Leu Ala Ala
 100 105 110
 Gly Ala Asp Val Ser Met Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser
 115 120 125
 Ala Tyr Pro Cys Ala Glu Arg Val Xaa Val Thr Ser Lys His Asn Asp
 130 135 140
 Asp Glu Gln Tyr Gly Gly Glu Xaa Gln Ala Gly Trp Leu Leu Tyr Cys
 145 150 155 160
 Gly His Val Ile Leu Leu Glu Ser Pro Phe Gly Gly Val Leu Arg Ser
 165 170 175
 Pro Ser Thr Ser Arg Thr Asn Ser Trp Ser Thr Leu Glu Arg Arg Ala
 180 185 190
 Phe Lys Asp Leu Gly Lys Asn Thr Pro Ser Ser
 195 200

<210> 46
 <211> 883
 <212> DNA
 <213> Hordeum vulgare

<220>
 <223> barley_13256964_HVSMEi0014B12f

<220>
 <221> modified_base
 <222> (1)..(883)
 <223> n = g, a, c or t

<400> 46
 cgagaacccc gctccaaagc cctaacccta ggccatcccc tctccctccc ctcaaccctc 60
 gtcgactccg cgcgcgcctg cgttccagga gcttcgcgtg ccggcggcgc catggcctca 120
 gagaccgaga ccttcgcctt ccaggcggag atcaaccagc tgctctcgct catcatcaac 180
 accttctact ccaacaagga gatcttccctc cgcgagctca tctccaacgc ctccgatgcg 240
 ttggataaga tcaggtttga gagcctcact gacaagagca agctggatgc tcagccagag 300
 ctgttcatcc acattatccc tgacaaggcc accaacacac tcacccttat cgacagtggc 360
 attggtatga ccaagtcaga cctcgtgaac aaccttggtg ccattgcaag gtctggcacc 420
 aaggatttca tggaggcatt ggctgctggt gccgatgtgt ccatgattgg tcagtttggg 480
 gttggtttct actctgctta cccttggtgct gagagagtcg ntgtgaccag caagcacaac 540
 gatgacgagc agtatggggg ggagtnccag gctgggtggc ttctttactg tggacacgtg 600
 atactcttgg agagcccctt tggaggggta ctaagatccc cctctacctc aaggacgaac 660
 agttggagta ccttggagag gcgcgccttt aaggatttgg ggaaaaacac tccgagttca 720
 taactttttc atctcctctg gacggggaaa acccctgaaa aggaattttt gcgctggaaa 780
 gtgggtggaa aaatgggttc ctgggggggc ccggttgagg gattgttggg cacataaaca 840
 actatcgtct tctatcttag cacctaatag tccttcacat gag 883

<210> 47
 <211> 164
 <212> PRT
 <213> Zea mays

<220>
 <223> corn BE511860

<400> 47
 Leu Leu Glu Gly Phe Glu Gln Arg Glu Pro Asp Asp Pro Cys Pro Tyr
 1 5 10 15
 Leu Leu Ser Ile Trp Thr Pro Gly Glu Thr Ala Gln Ser Ile Asp Ala
 20 25 30
 Pro Lys Thr Phe Cys Asp Ser Gly Glu Thr Gly Arg Leu Cys Gly Ser
 35 40 45
 Ser Thr Cys Phe Ser Cys Asn Asn Ile Arg Glu Met Gln Ala Gln Lys
 50 55 60
 Val Arg Gly Thr Leu Leu Ile Pro Cys Arg Thr Ala Met Arg Gly Ser
 65 70 75 80
 Phe Pro Leu Asn Gly Thr Tyr Phe Gln Val Asn Glu Val Phe Ala Asp
 85 90 95
 His Cys Ser Ser Gln Asn Pro Ile Asp Val Pro Arg Ser Trp Ile Trp
 100 105 110
 Asp Leu Pro Arg Arg Thr Val Tyr Phe Gly Thr Ser Val Pro Thr Ile
 115 120 125
 Phe Arg Gly Leu Thr Thr Glu Glu Ile Gln Arg Cys Phe Trp Arg Gly
 130 135 140
 Phe Val Cys Val Arg Gly Phe Asp Arg Thr Val Arg Ala Pro Arg Ala
 145 150 155 160
 Leu Tyr Ala Arg

<210> 48
 <211> 517
 <212> DNA
 <213> Zea mays

<220>
 <223> corn BE511860 EST946063H01.Y1 946

<400> 48
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 tccctgtcca tatcttcttt ccatatggac cccaggtgaa actgcacaat cgatcgatgc 120
 ccccaagaca ttctgtgatt caggggagac gggtagacta tgtggaagtt caacatgctt 180
 tagttgcaac aatatacgag aaatgcaggc tcagaaagtc agaggaacac ttttgatacc 240
 atgccgaaca gcaatgagag gaagcttccc acttaatggg acgtattttc aagttaatga 300
 ggtatttgct gaccattgct caagtcaaaa tccaattgat gtcccacgaa gttggatttg 360
 ggacctccca agacgaactg tttacttttg aacctcagtt cctacaatat tcagagggtt 420
 aacgactgaa gagatacaac gatgcttttg gagaggattt gtttgctgta ggggctttga 480
 taggacagtg cgggcaccaa gggcccttta tgcaagg 517

<210> 49
 <211> 137
 <212> PRT
 <213> Gossypium arboreum

<220>
 <223> cotton 11206330

<400> 49
 Met Gln Gly Asn Met Glu Leu Gln Glu Gly Asp Leu Ser Lys Ala Leu
 1 5 10 15
 Val Ala Leu Asn Pro Asp Ala Ala Ser Ile Pro Thr Pro Lys Leu Lys
 20 25 30
 Asn Val Ser Arg Leu Arg Thr Glu His Tyr Val Tyr Glu Leu Pro Asp
 35 40 45
 Lys His Pro Leu Leu Lys Gln Met Glu Lys Arg Glu Pro Asp Asp Pro
 50 55 60
 Ser Pro Tyr Leu Leu Ala Ile Trp Thr Pro Gly Glu Thr Ala Asn Ser
 65 70 75 80
 Ile Gln Pro Pro Glu Gln Ser Cys Gly Ser Gln Glu Pro Gly Arg Leu
 85 90 95
 Cys Asn Glu Lys Thr Cys Phe Ala Cys Asn Ser Val Arg Glu Ala Asn
 100 105 110
 Thr Glu Thr Val Arg Gly Thr Ile Leu Ile Pro Cys Arg Asn Ala Met
 115 120 125
 Arg Gly Ser Phe Ser Leu Asn Gly Thr
 130 135

<210> 50
 <211> 766
 <212> DNA
 <213> Gossypium arboreum

<220>
 <223> cotton 11206330 GA_Eb0023J04f

<400> 50
 ctccgccagt gcataacttg cttaaagtag ggcctaattg tggcaacaat gaacctatca 60
 ttgaggagcc tgcaacacct gaaccagagc atgcagaagg atcagagagt gatattgaag 120
 atgcaagcta tgatgatcca gatgaaattc ccacaataaa actcaacatt gaagagtcca 180
 cagcaaacct acagcattac atgcagggca atatggaact ccaagaaggg gacttgtcaa 240
 aggttttagt agctttgaat cctgatgctg cttctatccc tactccaaaa ttgaagaatg 300
 taagcaggct acgaacagag cactatgtat atgagcttcc agataaacat cctctcttga 360
 aacagatgga aaagcgggaa cctgatgatc ctagccccta tcttcttgca atatggacac 420
 caggtgaaac tgcaaaactca attcaaccac cagaacaaaag ttgtgggtcc caagaaccag 480
 gaagactgtg caatgagaag acctgctttg cttgcaacag tgtaagagaa gctaacactg 540
 agacagtccg aggaaccatc ttgatacctt gtagaaatgc aatgagagga agcttttccc 600
 ttaattggac ttaattttca agttaatgag gtcttttgca gatcatgaat caagcctcaa 660
 cccaatcgac gttccaaggg gaatggattg ggaatttaac aagaacgaac tgtataactg 720
 gaacatcctg gttcatcaat atttaaagga cttttcgacg agggaa 766

<210> 51
 <211> 179
 <212> PRT
 <213> Glycine max

<220>
 <223> soybean 5606759

<220>
 <221> MOD_RES
 <222> (167)
 <223> Xaa = His or Gln

<400> 51
 Met Gly Trp Val Pro Leu Gln Pro Leu Pro Glu Ser Leu Gln Leu His
 1 5 10 15
 Leu Leu Glu Leu Tyr Pro Val Leu Glu Ser Ile Gln Lys Tyr Leu Trp
 20 25 30
 Pro Arg Leu Cys Lys Leu Asp Gln Glu Thr Leu Tyr Glu Leu His Tyr
 35 40 45
 Gln Met Ile Thr Phe Gly Lys Val Phe Cys Thr Lys Ser Lys Pro Asn
 50 55 60
 Cys Asn Ala Cys Pro Met Arg Ala Glu Cys Arg His Phe Ala Ser Ala
 65 70 75 80
 Phe Ala Ser Ala Arg Phe Ala Leu Pro Gly Pro Glu Gln Lys Ser Ile
 85 90 95
 Val Ser Thr Thr Gly Asn Ser Val Ile Asn Gln Asn Pro Ser Glu Ile
 100 105 110
 Ile Ser Gln Leu His Leu Pro Pro Pro Glu Asn Thr Ala Gln Glu Asp
 115 120 125
 Glu Ile Gln Leu Thr Glu Val Ser Arg Gln Leu Glu Ser Lys Phe Glu
 130 135 140
 Ile Tyr Ile Cys Gln Pro Ile Ile Glu Glu Pro Arg Thr Pro Glu Pro
 145 150 155 160
 Glu Cys Leu Gln Glu Ser Xaa Thr Asp Ile Glu Asp Ala Val Tyr Glu
 165 170 175
 Asp Ser Ser

<210> 52
 <211> 583
 <212> DNA
 <213> Glycine max

<220>
 <223> soybean 5606759 sb95c12.y1

<220>
 <221> modified_base
 <222> (546)
 <223> n = g, a, c or t

<400> 52
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 ctgcagccac tgcctgagtc actgcagttg catctcctag aattgtaccc ggtgttgag 120
 tcaatacaaaa aatatctctg gcctcgactg tgcaagctag atcaggaaac actatatgag 180
 ctacattacc agatgattac atttggaag gtcttctgta caaaaagcaa accaaattgt 240
 aatgcatgcc caatgagagc agaatgtaga cactttgcta gtgcatttgc aagtgaagg 300
 tttgcactgc ctggaccaga gcagaagagt atagtttagca caactggaaa tagtgtgatt 360
 aaccagaacc catctgaaat catcagtcag ttgcacttgc ctccacctga gaacacagcc 420
 caagaagatg aaattcaact aacagaagtg agcagacaat tggaatcaaa atttgaaata 480
 tatatttgcc aacctatcat tgaagagccc agaactccag agccagaatg cttgcaagaa 540
 tcacanactg atatagagga tgctgtctat gaggattcaa gtg 583

<210> 53
 <211> 155
 <212> PRT
 <213> Triticum aestivum

<220>
 <223> wheat 12019155

<400> 53
 Met Phe His Cys His Gly Thr Arg Gly Ser Asp Leu Gly Phe Asp Leu
 1 5 10 15
 Asn Lys Thr Pro Glu Gln Lys Ala Pro Gln Arg Arg Lys His Arg Pro
 20 25 30
 Lys Val Ile Lys Glu Ala Lys Pro Lys Ser Thr Arg Lys Pro Ala Thr
 35 40 45
 Gln Lys Thr Gln Met Lys Glu Asn Pro His Lys Lys Arg Lys Tyr Val
 50 55 60
 Arg Lys Thr Ala Ala Thr Pro Gln Thr Asn Val Thr Glu Glu Ser Val
 65 70 75 80
 Asp Ser Ile Val Ala Thr Lys Lys Ser Cys Arg Arg Ala Leu Asn Phe
 85 90 95
 Asp Leu Glu His Asn Lys Tyr Ala Ser Gln Ser Thr Ile Ser Cys Gln
 100 105 110
 Gln Glu Ile Asp His Arg Asn Glu Lys Ala Phe Asn Thr Thr Ser Asp
 115 120 125
 His Lys Ala Lys Glu Pro Lys Asn Thr Asp Asp Asn Thr Leu Leu Leu
 130 135 140
 His Glu Lys Gln Ala Asn Asn Phe Gln Ser Glu
 145 150 155

<210> 54
 <211> 902
 <212> DNA
 <213> Triticum aestivum

<220>
 <223> wheat 12019155 ESTBRY_901

<220>
 <221> modified_base
 <222> (1)..(902)
 <223> n = g, a, c or t

<400> 54
 aacagtcagg acaaaggcaa caagatcagc agtcaggaca agggcagcaa ccgggacaaa 60
 ggcagccagg gtactactca acttctccgc aacaattagg acaaggccaa ccaaggtact 120
 acccaacttc tccgcagcag ccaggacaag agcagcagcc aagacaattg caacaaccag 180
 aacaagggca acaaggtcag cagccagaac aagggcagca aggtcagcag caaagacaag 240
 gggagcaagg tcagcagcca ggacaagggc aacaagggca gcaaccggga caagggcagc 300
 caggggtacta cccaacttct cgcagcagc caggacaagg gcaaccaggg tactacccaa 360
 cttctccaca gcagtcagga caattgcaac aaccagcaca agggcagcaa ccaggacaag 420
 agcaacaagg tcaacagcca ggacaagggc agcaaccggg acaagggcaa gccagggtac 480
 taccgaactt ctccgcagca gtcaggacaa gagcaacagc tagaacaatg gcaacagtca 540
 ggacaggggc aaccagggca ctaccaact tctccgttgc aagccaggac aagggcaacc 600
 aggggtactac ccaacttctc acaacagata ggacaagggc agcagccaag aacaatttgc 660
 acaaccaaca caagggcaac aangggcagc aaccaaggac aangggcaac aaggtcaaca 720
 gcccangaaa aaaggcaaca aaggtcaagc aaccaagnac aaggggcagc aanccaggac 780
 aagggcagcc anggtcctac ccaacttntt ttgagcaagt canggaaaag gggcaccanc 840
 cnagganaaa tgggnaccac ccagnacaag gacaaccccg ggtcttcccc aaantttttn 900
 cn 902

<210> 55
 <211> 255
 <212> PRT
 <213> Lycopersicon esculentum

<220>
 <223> tomato 8106032

<220>
 <221> MOD_RES
 <222> (1)..(255)
 <223> Xaa = any amino acid

<400> 55
 Met Ser Leu Ala Ala His Phe Pro Leu Lys Thr Asp Ser Thr Gln Lys
 1 5 10 15
 His Glu Gly Asn Thr Gly Ile Ile Ile Glu Glu Pro Glu Glu Cys Ala
 20 25 30
 Thr Asp Pro Asn Val Ser Ile Arg Trp Tyr Glu Asp Gln Pro Asn Gln
 35 40 45
 Ser Thr His Cys Gln Asp Ser Ser Gly Val Tyr Asn Thr Asp Ser Asn
 50 55 60
 Glu Glu Lys Pro Ala Val Asn Asp Ser Glu Ser Ser Glu Asn Ser Thr
 65 70 75 80

Glu Cys Ile Lys Ser Ala Glu Cys Ser Val Ile Leu Gln Ser Asp Ser
 85 90 95
 Ser Arg Glu Gly Ser Asp Leu Tyr His Gly Ser Thr Val Thr Ser Ser
 100 105 110
 Gln Asp Arg Lys Glu Leu Asn Asp Leu Pro Ser Ser Pro Ser Ser Val
 115 120 125
 Val Ser Ser Glu Ile Ser Ala Val Ile Gln Ala Ser Glu Gly Thr Asp
 130 135 140
 Ser Ser Asn Phe Cys Ser Ser Thr Ser Phe Leu Lys Leu Leu Gln Met
 145 150 155 160
 Ala Gly Thr Ser Gly Ala Gln Gly Thr Arg Cys Thr Glu His Leu His
 165 170 175
 Asn Gln His Lys Gly Asn Xaa Gly Gln Gln Pro Arg Thr Xaa Gly Asn
 180 185 190
 Lys Val Asn Ser Pro Xaa Lys Lys Ala Thr Lys Val Lys Gln Pro Xaa
 195 200 205
 Thr Arg Gly Ser Xaa Pro Gly Gln Gly Gln Pro Xaa Ser Tyr Pro Thr
 210 215 220
 Xaa Phe Glu Gln Val Xaa Glu Lys Gly His Xaa Pro Arg Xaa Asn Gly
 225 230 235 240
 Xaa His Pro Xaa Gln Gly Gln Pro Arg Val Phe Pro Lys Xaa Phe
 245 250 255

<210> 56
 <211> 589
 <212> DNA
 <213> Lycopersicon esculentum

<220>
 <223> tomato 8106032 EST356474

<400> 56
 ctcggtgccgg ttgggggtata tcttacacag aatgttttcag atcacctttc tagttctgca 60
 ttcattgtcac tcgctgccc ctttctctg aaaacagaca gtactcagaa gcatgaagga 120
 aatacaggta ttataattga agaacctgaa gagtgtgcaa cagaccccaa tgtttccatc 180
 agatgggtatg aagatcaacc aaatcagtc acccattgtc aggattcttc aggagtctat 240
 aatacagatt caaatgaaga aaaaccagct gtcaatgact ctgaatcaag tgaaaatagc 300
 acagaatgca taaaatcagc agaatgttct gtaattctgc aatcagattc ttctagagaa 360
 ggctcagatc tgtatcatgg atcaacagtt acaagttccc aagatcgaaa agagttgaat 420
 gatttgccct cttctccgag ttctgttggt tcttctgaga tctctgctgt tattcaagct 480
 tcagaaggaa ctgactcaag caacttttgc agctccactt cttttttgaa gctattacag 540
 atggcaggaa cttcaggagc acaaggaacc aggtgcactg aacatctac 589

<210> 57
 <211> 179
 <212> PRT
 <213> Zea mays

<220>

<223> corn AW042334

<400> 57

Asp Ala His Pro Leu Leu Gln Gln Leu Gly Leu Asp Gln Arg Glu His
1 5 10 15

Asp Asp Pro Thr Pro Tyr Leu Leu Ala Ile Trp Thr Pro Asp Gly Ile
20 25 30

Lys Glu Ile Thr Lys Thr Pro Lys Pro Cys Cys Asp Pro Gln Met Gly
35 40 45

Gly Asp Leu Cys Asn Asn Glu Met Cys His Asn Cys Thr Ala Glu Lys
50 55 60

Glu Asn Gln Ser Arg Tyr Val Arg Gly Thr Ile Leu Val Pro Cys Arg
65 70 75 80

Thr Ala Met Arg Gly Ser Phe Pro Leu Asn Gly Thr Tyr Phe Gln Val
85 90 95

Asn Glu Val Phe Ala Asp His Arg Ser Ser His Asn Pro Ile His Val
100 105 110

Glu Arg Glu Met Leu Trp Asn Leu Gln Arg Arg Met Val Phe Phe Gly
115 120 125

Thr Ser Val Pro Thr Ile Phe Lys Gly Leu Arg Thr Glu Glu Ile Gln
130 135 140

Gln Cys Phe Trp Arg Gly Phe Val Cys Val Arg Gly Phe Asp Met Glu
145 150 155 160

Thr Arg Ala Pro Arg Pro Leu Cys Pro His Leu His Val Ile Ala Arg
165 170 175

Pro Lys Ala

<210> 58

<211> 595

<212> DNA

<213> Zea mays

<220>

<223> corn AW042334 EST614027C01.y1 614

<400> 58

gaattcggca ccagcagatg cacatccact tttacaacag ctaggacttg accaacggga 60
acatgatgat cctaccccat acttattggc catatggaca ccagatggaa taaaggaaat 120
aactaagaca ccaaaaccat gctgtgaccc tcaaattggga ggcgatttat gcaataatga 180
aatgtgccac aattgtactg cagagaaaga aaaccaatct agatatgtca gaggcacaat 240
tctggttcct tgtcgaacag ctatgagggg tagtttccca cttaatggca cttactttca 300
agtcaatgag gtatttgctg accacagatc tagccacaac ccaatccatg tggaaaggga 360
gatgctatgg aacttgcaaa ggcgcattgg ctttttcggg acttcagtac ccaccatatt 420
caaaggtcta agaacagaag aaatacaaca atgcttctgg aggggatttg tctgtgtgcg 480
aggattcgac atggagacta gagcaccaag gcctctgtgc ccccatattgc acgttatagc 540
aaggccgaaa gcccgcaaga cagcagcaac tgagcaagta ctctaatacag caaag 595

<210> 59
 <211> 150
 <212> PRT
 <213> Zea mays

<220>
 <223> corn AW076298

<400> 59
 Pro Cys Arg Thr Ala Met Arg Gly Ser Phe Pro Leu Asn Gly Thr Tyr
 1 5 10 15
 Phe Gln Val Asn Glu Val Phe Ala Asp His Cys Ser Ser Gln Asn Pro
 20 25 30
 Ile Asp Val Pro Arg Ser Trp Ile Trp Asp Leu Pro Arg Arg Thr Val
 35 40 45
 Tyr Phe Gly Thr Ser Val Pro Thr Ile Phe Arg Gly Leu Ser Thr Glu
 50 55 60
 Gln Ile Gln Phe Cys Phe Trp Lys Gly Phe Val Cys Val Arg Gly Phe
 65 70 75 80
 Glu Gln Lys Thr Arg Ala Pro Arg Pro Leu Met Ala Arg Leu His Phe
 85 90 95
 Pro Ala Ser Lys Leu Lys Asn Asn Lys Leu Thr Thr Glu Glu Ile Gln
 100 105 110
 Gln Cys Phe Trp Arg Gly Phe Val Cys Val Arg Gly Phe Asp Arg Thr
 115 120 125
 Val Arg Ala Pro Arg Pro Leu Tyr Ala Arg Leu His Phe Pro Ala Ser
 130 135 140
 Lys Val Val Arg Gly Lys
 145 150

<210> 60
 <211> 640
 <212> DNA
 <213> Zea mays

<220>
 <223> corn AW076298 EST614065C03.y1 614

<400> 60
 cggccccaga ccatgccgga cagcaatgag aggaagcttc ccacttaatg ggacatatatt 60
 tcaagttaat gaggtatttg ctgaccattg ttcaagccaa aatccaattg atgtcccacg 120
 aagttggata tgggacctcc caagacgaac tgtttacttt ggaacctcag ttcctacaat 180
 atttagaggt ttaacgactg aagagataca acaatgcttt tggagaggat tcgttttgtgt 240
 gaggggcttt gataggacag taagggcacc aaggccctt tatgcaaggt tgcattttcc 300
 tgccagcaag gttgttagag gcaaaaagcc tggagcggca agcgtcgaag aataataggt 360
 acatcgaaga aatatagagg agctaacaaa acggatggat agccctaaat gagatgctga 420
 cccaataagt cgccgaatca cctccaagtt ctaacccaat ttttgaggcg acatgacctg 480
 ttaaattatg ttccatctat ggtaacagct tagatgttct tgtgagtcgc atattcttta 540
 ctctgaaatt caatatagca aatgaaaaaa aacacagtgc atagtctagt tctaattgta 600
 cctgtgagtg gaatcagttg ttgtacaaca tgaagatggg 640

<210> 61
 <211> 140
 <212> PRT
 <213> Zea mays

<220>
 <223> corn BE639158

<400> 61
 Lys Asn Ser Glu Pro Ile Ile Glu Glu Pro Ala Ser Pro Arg Glu Glu
 1 5 10 15
 Arg Pro Pro Glu Thr Met Glu Asn Asp Ile Glu Asp Phe Tyr Glu Asp
 20 25 30
 Gly Glu Ile Pro Thr Ile Lys Leu Asn Met Glu Ala Phe Ala Gln Asn
 35 40 45
 Leu Glu Asn Cys Ile Lys Glu Ser Asn Asn Glu Leu Gln Ser Asp Asp
 50 55 60
 Ile Ala Lys Ala Leu Val Ala Ile Ser Thr Glu Ala Ala Ser Ile Pro
 65 70 75 80
 Val Pro Lys Leu Lys Asn Val Leu Arg Leu Arg Thr Glu His Tyr Val
 85 90 95
 Tyr Glu Leu Pro Asp Ala His Pro Leu Leu Gln Gln Leu Gly Leu Asp
 100 105 110
 Gln Arg Glu His Asp Asp Pro Thr Pro Tyr Leu Leu Ala Ile Trp Thr
 115 120 125
 Pro Asp Gly Ile Lys Glu Ile Thr Lys Thr Pro Lys
 130 135 140

<210> 62
 <211> 561
 <212> DNA
 <213> Zea mays

<220>
 <223> corn BE639158 EST946021E09.y1 946

<400> 62
 tgagctgcat tatcagatga ttacatttgg aaaggtcttt tgtaccacaaa gacagccaaa 60
 ttgcaatgca tgctatgaat tcgactcacc tacctcgccct tgaggggagat atccattcaa 120
 gggagtttct tcctaagaat tcagagccaa taatcgagga gcctgcaagt ccaagagagg 180
 aaagacctcc agaaaccatg gaaaatgata ttgaagattt ttatgaagat ggtgaaatcc 240
 caacaataaaa gcttaacatg gaagcttttg cacaaaactt ggagaattgc attaaagaaa 300
 gcaataacga actccagtct gatgatattg caaaagcatt ggttgctatt agcactgaag 360
 cagcttcgat tcctgtaccg aaactaaaga atgtgcttag gcttcgaaca gaacactatg 420
 tgtatgagct tccagatgca catccacttt tacaacagct aggacttgac caacgggaac 480
 atgatgatcc taccatac ttattggcca tatggacacc agatggaata aaggaaataa 540
 ctaagacacc aaaaccatgc t 561

<210> 63
 <211> 138
 <212> PRT
 <213> Zea mays

<220>
 <223> corn T25243

<220>
 <221> MOD_RES
 <222> (63)
 <223> Xaa = Asp or Glu

<220>
 <221> MOD_RES
 <222> (114)
 <223> Xaa = Cys, Trp, Arg, Ser or Gly

<400> 63
 Asn His Gln Pro Ile Ile Glu Glu Pro Leu Ser Pro Glu Cys Glu Thr
 1 5 10 15
 Glu Asn Ile Glu Ala His Glu Gly Ala Ile Glu Asp Phe Phe Cys Glu
 20 25 30
 Glu Ser Asp Glu Ile Pro Thr Ile Asn Leu Asn Ile Glu Glu Phe Thr
 35 40 45
 Gln Asn Leu Lys Asp Tyr Met Gln Ala Asn Asn Val Glu Ile Xaa Tyr
 50 55 60
 Ala Asp Met Ser Lys Ala Leu Val Ala Ile Thr Pro Asp Ala Ala Ser
 65 70 75 80
 Ile Pro Thr Pro Lys Leu Lys Asn Val Asn Arg Leu Arg Thr Glu His
 85 90 95
 Gln Val Tyr Glu Leu Pro Asp Ser His Pro Leu Leu Glu Gly Phe Glu
 100 105 110
 Gln Xaa Glu Pro Asp Asp Pro Cys Pro Tyr Leu Leu Ser Ile Trp Thr
 115 120 125
 Pro Gly Glu Leu His Asn Arg Ser Met Pro
 130 135

<210> 64
 <211> 422
 <212> DNA
 <213> Zea mays

<220>
 <223> corn T25243 EST5c10h02

<220>
 <221> modified_base
 <222> (1)..(422)
 <223> n = g, a, c or t

<400> 64
ctggtaatca tcagccaatc atcgaggaac cactgagccc agaatgtgaa actgaaaata 60
tagaggcaca tgaggggtgca attgaggatt tcttttgtga agaattctgat gaaattccta 120
ccattaatct taatatcgag gagttcacac aaaacttgaa ggactatatg caagcaaaca 180
atggttgagat tgantatgct gacatgtcaa aggcattggt tgccatcacg cctgatgctg 240
cttccattcc aactccaaag ctcaagaatg tcaatcgtct gaggacagaa caccaagttt 300
atgaactgcc agattcacac cctcttctgg aaggattcga acagngngaa ccagatgatc 360
cctgtccata tcttctttcc atatggaccc caggtgaact gcacaatcga tcgatgcccc 420
aa 422

<210> 65
<211> 89
<212> PRT
<213> Zea mays

<220>
<223> corn AW453174

<400> 65
Phe Gln Gly Asn Glu Val Phe Ala Asp His Cys Ser Arg Gln Asn Pro
1 5 10 15
Ile Asp Gly Pro Arg Ser Trp Ile Trp Asp Leu Pro Arg Arg Thr Gly
20 25 30
Tyr Phe Gly Thr Ser Gly Pro Thr Ile Phe Arg Gly Leu Thr Thr Glu
35 40 45
Glu Ile Gln Arg Cys Phe Trp Arg Gly Phe Val Cys Val Arg Gly Phe
50 55 60
Asp Arg Thr Val Arg Ala Pro Arg Pro Leu Tyr Ala Arg Leu His Phe
65 70 75 80
Pro Val Ser Lys Val Val Arg Gly Lys
85

<210> 66
<211> 488
<212> DNA
<213> Zea mays

<220>
<223> corn AW453174 EST 660032D01.y1 660

<400> 66
catgccgaac agcaatgaga ggaagcttcc cacttaatgg gacgattttc aaggtaatga 60
ggtattttgct gaccattgct caaggcaaaa tccaattgat ggcccacgaa gttggatttg 120
ggaccttcca agacgaactg gttacttttg aacctcaggt cctacaatat tcagagggtt 180
aacgactgaa gagatacaac gatgcttttg gagaggattt gtttgctgta ggggctttga 240
taggacagtg cgggcaccaa ggccccttta tgcaagggtg cattttcctg tcagcaaggt 300
tgtttagaggc aaaaagcctg gagcagcaag agcagaagaa taatagaaca ttgaagaaat 360
ataggggtgc taaccagatg aggatggata gcccgaatg agatgctgac ccaataggtc 420
gccaaatcac ctccaaattc taacccaatg acttccatct gtaatgaatg gcaatacctt 480
gaaaacct 488

<210> 67
 <211> 93
 <212> PRT
 <213> Zea mays

<220>
 <223> corn BE509759

<400> 67
 Asn Gly Thr Tyr Phe Gln Val Asn Glu Val Phe Ala Asp His Arg Ser
 1 5 10 15
 Ser His Asn Pro Ile His Val Glu Arg Glu Met Leu Trp Asn Leu Gln
 20 25 30
 Arg Arg Met Val Phe Phe Gly Thr Ser Val Pro Thr Ile Phe Lys Gly
 35 40 45
 Leu Arg Thr Glu Glu Ile Gln Gln Cys Phe Trp Arg Gly Phe Val Cys
 50 55 60
 Val Arg Gly Phe Asp Met Glu Thr Arg Ala Pro Arg Pro Leu Cys Pro
 65 70 75 80
 His Leu His Ile Ile Ala Arg Pro Lys Ala Arg Lys Thr
 85 90

<210> 68
 <211> 570
 <212> DNA
 <213> Zea mays

<220>
 <223> corn BE509759 EST946021E09.x1 946

<400> 68
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 aaagtgaaaa ttattgggtgc ttcttgatgc ttcatatagtc ctctcgtctc agaaactaac 120
 agtctcggac cccatccatg gcttaaattt cctaaacaat ggctcttttt taggcaggaa 180
 gtaatatgat tccatgcata ggctgagagc tattgatgtc atatcacaat aaacatgatg 240
 ttcataaaac tgatatcttt gctgattaga gtacttgctc agttgctgct gtcttgcggg 300
 ccttcggcct tgctataatg tgcaaattggg ggcacagagg ccttggtgct ctagtctcca 360
 tgtcgaatcc tcgcacacag acaaatcccc tccagaagca ttgttgattt tcttctgttc 420
 ttagaccttt gaatatggtg ggtactgaag tcccgaaaaa gaccatgcgc ctttgcaagt 480
 tccatagcat ctccctttcc acatggattg gggtgtggct agatctgtgg tcagcaaata 540
 cctcattgac ttgaaagtaa gtgccattaa 570

<210> 69
 <211> 71
 <212> PRT
 <213> Zea mays

<220>
 <223> corn AW017984

<400> 69
 Val Pro Arg Ser Trp Ile Trp Asp Leu Pro Arg Arg Thr Val Tyr Phe
 1 5 10 15

Gly Thr Ser Val Pro Thr Ile Phe Arg Gly Leu Thr Thr Glu Glu Ile
 20 25 30

Gln Gln Cys Phe Trp Arg Gly Phe Val Cys Val Arg Gly Phe Asp Arg
 35 40 45

Thr Val Arg Ala Pro Arg Pro Leu Tyr Ala Arg Leu His Phe Pro Ala
 50 55 60

Ser Lys Val Val Arg Gly Lys
 65 70

<210> 70
 <211> 613
 <212> DNA
 <213> Zea mays

<220>
 <223> corn AW017984 EST614065C03.x1 614

<400> 70
 cctgaaacaa tcaaataacg gccgatgagg ttacattggt tatagtatat gatcaaagaa 60
 catgtatgac cattgtacaa ataggcccat cttcatgttg tacaacaact gattccactc 120
 acaggtagaa ttagaactag actatgcact gtgttttttt tcatttgcta tattgaattt 180
 cagagtaaag aatatgagac tcacaagaac atctaagctg ttaccataga tggaacataa 240
 tttaacaggt catgtcgcct caaaaatttg gttagaactt ggagggtgatt cggcgactta 300
 ttgggtcagc atctcattta gggctatcca tccgttttgt tagctcctct atatttcttc 360
 gatgtacctt ttattcttcg acgcttgccg ctccaggctt tttgcctcta acaaccttgc 420
 tggcaggaaa atgcaacctt gcataaaggg gccttggtgc ccttactgtc ctatcaaagc 480
 ccctcacaca aacgaatcct ctccaaaagc attgttgat ctcttcagtc gttaaacttc 540
 taaatattgt aggaactgag gttccaaagt aaacagttcg tcttgggagg tcccatatcc 600
 aacttcgtgg gac 613

<210> 71
 <211> 90
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DMT Domain A
 consensus sequence

<220>
 <221> MOD_RES
 <222> (3)
 <223> Xaa = any amino acid

<220>
 <221> MOD_RES
 <222> (4)
 <223> Xaa = Ile or Leu

<220>
 <221> MOD_RES
 <222> (6)
 <223> Xaa = Asp or Pro

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<220>
<221> MOD_RES
<222> (7)
<223> Xaa = Glu or Val

<220>
<221> MOD_RES
<222> (9)..(11)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (13)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (14)
<223> Xaa = Leu or Val

<220>
<221> MOD_RES
<222> (16)
<223> Xaa = Met or Leu

<220>
<221> MOD_RES
<222> (17)
<223> Xaa = Glu or Asp

<220>
<221> MOD_RES
<222> (18)..(19)
<223> Xaa = any amino acid, Xaa at positions 18 and 19
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 Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Arg Xaa
 20 25 30
 Xaa Phe Xaa Xaa Arg Xaa Xaa Xaa Phe Ile Xaa Arg Met Xaa Xaa Xaa
 35 40 45

Gln Gly Xaa Arg Xaa Phe Xaa Xaa Trp Lys Gly Ser Val Val Asp Ser
 50 55 60
 Val Xaa Gly Val Phe Leu Thr Gln Asn Xaa Asp Xaa Xaa Ser Ser Xaa
 65 70 75 80
 Ala Xaa Met Xaa Xaa Ala Xaa Xaa Phe Pro
 85 90

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 20 25 30
 Xaa Xaa Xaa Xaa Ile Xaa Xaa Arg Gly Xaa Xaa Xaa Xaa Leu Xaa Xaa
 35 40 45
 Arg Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Leu
 50 55 60
 Xaa Xaa Xaa Val Xaa Xaa Xaa Gly Xaa Ile Asp Leu Glu Trp Leu Arg
 65 70 75 80
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Leu Leu Xaa Xaa Xaa Gly
 85 90 95
 Xaa Gly Leu Lys Ser Xaa Glu Cys Val Arg Leu Leu Xaa Leu Xaa Xaa
 100 105 110
 Xaa Ala Phe Pro Val Asp Thr Asn Val Gly Arg Ile Xaa Val Arg Xaa
 115 120 125
 Gly Xaa Val Pro Leu Xaa Pro Leu Pro Xaa Xaa Xaa Gln Xaa His Xaa
 130 135 140
 Leu Xaa Xaa Tyr Pro Xaa Xaa Xaa Xaa Xaa Gln Lys Xaa Leu Trp Pro
 145 150 155 160
 Arg Leu Cys Lys Leu Xaa Gln Xaa Thr Leu Tyr Glu Leu His Tyr Xaa
 165 170 175
 Xaa Ile Thr Phe Gly Lys Xaa Xaa Phe Cys Thr Lys Xaa Xaa Pro Asn
 180 185 190

Cys Asn Ala Cys Pro Met Xaa Xaa Xaa Glu Cys Xaa Xaa Xaa Xaa Ser
 195 200 205

Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa
 210 215 220

Xaa Xaa Leu Xaa Xaa Xaa
 225 230

<210> 73
 <211> 292
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<220>
 <223> Description of Artificial Sequence:DMT Domain C
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 May be present or absent

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 20 25 30

 Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45

 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Ile Xaa Xaa Xaa
 50 55 60

 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 65 70 75 80

 Xaa Xaa Xaa Xaa Leu Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro
 85 90 95

 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa Xaa Leu Arg Thr Glu
 100 105 110

His Xaa Val Xaa Xaa Leu Pro Asp Xaa His Xaa Xaa Leu Xaa Xaa Xaa
 115 120 125
 Asp Xaa Xaa Xaa Tyr Leu Leu Xaa Ile Trp Xaa Pro Xaa Xaa Xaa Xaa
 130 135 140
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa
 145 150 155 160
 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa
 165 170 175
 Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Arg Gly Thr Xaa Leu Xaa
 180 185 190
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 195 200 205
 Xaa Xaa Xaa Xaa Xaa Xaa Phe Ala Asp His Xaa Xaa Xaa Xaa Xaa Pro
 210 215 220
 Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Arg Xaa Xaa
 225 230 235 240
 Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Ile Xaa Xaa Xaa Leu Xaa Xaa Xaa
 245 250 255
 Xaa Ile Xaa Xaa Xaa Phe Xaa Xaa Gly Xaa Xaa Cys Xaa Arg Xaa Phe
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 275 280 285
 Xaa Xaa Ser Lys
 290

<210> 74
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<220>
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 sequence spanning Domains A, B and C

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 20 25 30
 Xaa Xaa Xaa Lys Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45
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 50 55 60
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 65 70 75 80
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 85 90 95
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 100 105 110
 Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 115 120 125
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 130 135 140
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 145 150 155 160
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 165 170 175

Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Val	Xaa	Xaa	Asp	Xaa	Xaa	Thr	Xaa	Xaa	Xaa	180	185	190	
Trp	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	195	200	205	
Xaa	Xaa	Glu	Arg	Xaa	Xaa	Phe	Xaa	Xaa	Arg	Xaa	Xaa	Xaa	Phe	Ile	Xaa	210	215	220	
Arg	Met	Xaa	Xaa	Xaa	Gln	Gly	Xaa	Arg	Xaa	Phe	Xaa	Xaa	Trp	Lys	Gly	225	230	235	240
Ser	Val	Val	Asp	Ser	Val	Xaa	Gly	Val	Phe	Leu	Thr	Gln	Asn	Xaa	Asp	245	250	255	
Xaa	Xaa	Ser	Ser	Xaa	Ala	Xaa	Met	Xaa	Xaa	Ala	Xaa	Xaa	Phe	Pro	Xaa	260	265	270	
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835 840 845
Thr Asn Val Gly Arg Ile Xaa Val Arg Xaa Gly Xaa Val Pro Leu Xaa
850 855 860
Pro Leu Pro Xaa Xaa Xaa Gln Xaa His Xaa Leu Xaa Xaa Tyr Pro Xaa
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Gln Xaa Thr Leu Tyr Glu Leu His Tyr Xaa Xaa Ile Thr Phe Gly Lys
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Xaa Xaa Phe Cys Thr Lys Xaa Xaa Pro Asn Cys Asn Ala Cys Pro Met
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 20 25 30

Val Asp

<210> 76
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 Xba-SKEN-7

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29

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<210> 78
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 <210> 89
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 <400> 89
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 <210> 90
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<210> 97
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 <220>
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 <210> 99
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 <220>
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 <210> 100
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 <210> 104
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 <210> 106
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 <210> 108
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 <210> 109
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 <220>
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 <400> 109
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 <210> 110
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 <220>
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 <210> 111
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 2.2+SKE-1

 <400> 111
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<210> 112
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 <210> 113
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 <400> 113
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 <210> 114
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 <210> 115
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 <210> 116
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<210> 117
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<210> 118
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<210> 119
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<212> DNA
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2.2+SKE-3

<400> 119
ccgtaaacaa caccggatac ac 22

*Q10
Amal*